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## Identifying transcripts associated with aggressiveness in wheat yellow rust by transcriptomic sequencing

Yan-Jun (Angie) Chen<sup>1</sup>, Josef Korbinian Vogt<sup>2</sup>, Chris Khadgi Sørensen<sup>1</sup>, Julian Rodriguez-Algaba<sup>1</sup>, Thomas Sicheritz-Ponten<sup>2</sup>, Mogens Støvring Hovmøller<sup>1</sup> & Annemarie Fejer Justesen<sup>1</sup>

<sup>1</sup>Aarhus University, Department of Agroecology, Faculty of Sciences and Technology, DK-4200 Slagelse, Denmark

<sup>2</sup>Center for Biological Sequence Analysis, Department of Systems Biology, Technical University of Denmark, Kemitorvet, Building 208, 2800 Lyngby, Denmark

Yellow rust (*Puccinia striiformis*) is currently one of the most prevalent and damaging disease on wheat, which may threaten global food security. This is emphasized by new strains adapted to warmer temperatures, and being more aggressive in general, which have spread rapidly in many wheat growing areas in recent years. More detailed knowledge is needed for understanding rust biology and epidemiology, e.g., the characteristics of aggressive isolates. Since 2011, the isolate DK09/11 of the “Warrior” race is considered ‘aggressive’ and spreading rapidly in Europe. In this study, progeny isolates arising from a selfing of the isolate DK09/11 on *Berberis vulgaris* (Rodriguez-Algaba J, et al., 2014) were selected for transcriptomic analysis. Four progeny isolates and the parent isolate DK09/11 showing different levels of aggressiveness were point inoculated on wheat leaves and harvested at three different time points (5, 7 and 9 dai) for RNA-sequencing. By using next-generation sequencing technologies, transcript expression profiles under different growth stages will be analyzed to reveal molecular mechanisms underlying aggressiveness.

Rodriguez-Algaba J, Walter S, Sørensen C K, Hovmøller MS & Justesen AF. 2014. Sexual structures and recombination of the wheat rust fungus *Puccinia striiformis* on *Berberis vulgaris*. *Fungal Genetics and Biology* 70, 77-85.